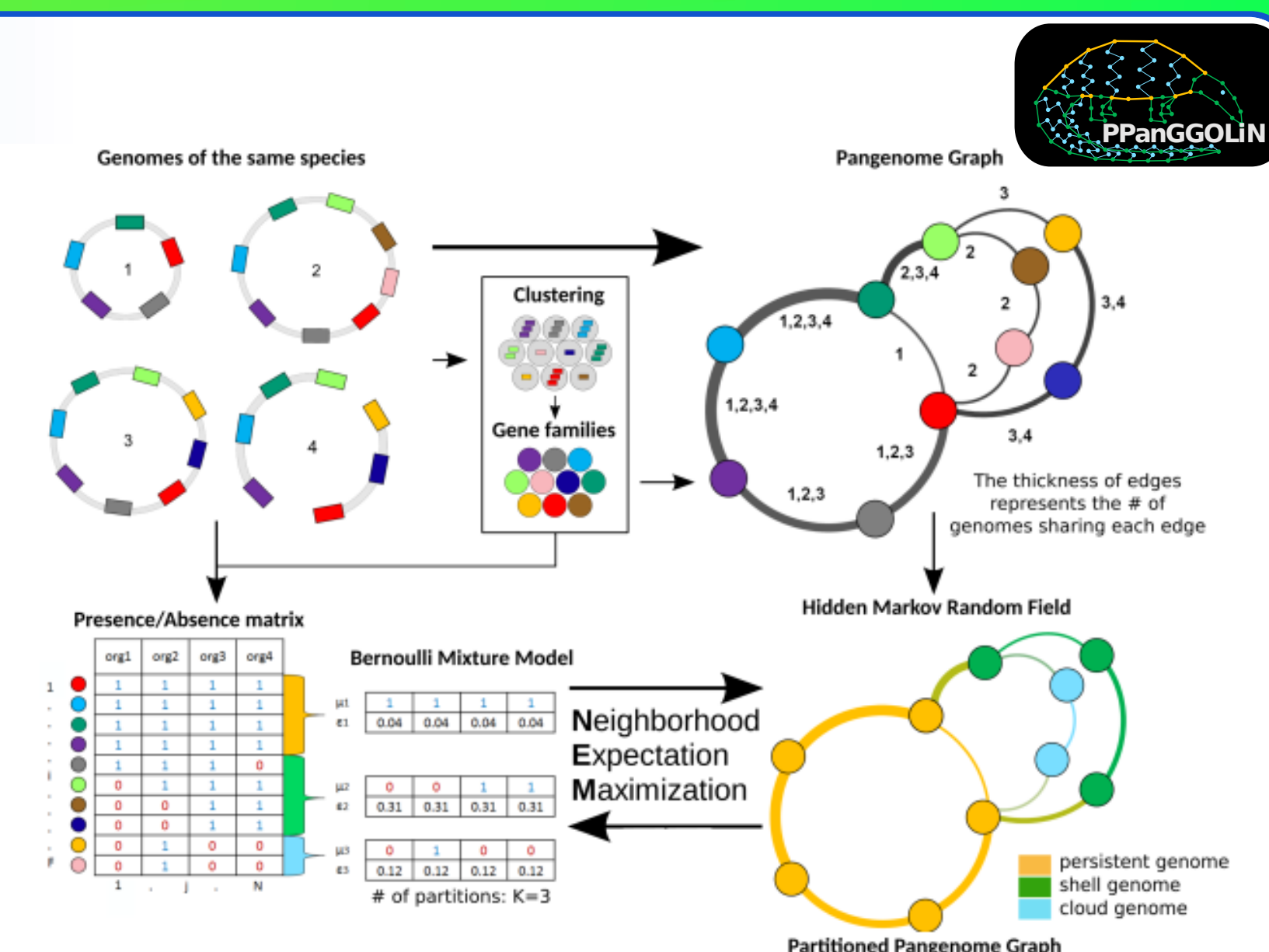


OUTLINE

PANORAMA is an open-source bioinformatics toolbox, including new methodological developments for the comparative study of pangenomes. It benefits from methods for the **reconstruction and analysis of pangenome graphs**, thanks to the **PPanGGOLIN**¹ software suite. PANORAMA integrates multiple features, such as the possibility to **compare genomic context** between pangenomes or the **annotation of biological systems** at the pangenome level.

PANORAMA allows comparative analysis of pangenomes using thousands of genomes. The software is developed in python and can be install with conda. It generates many tables and graphical outputs, some of them being compatible with external bioinformatic tools.

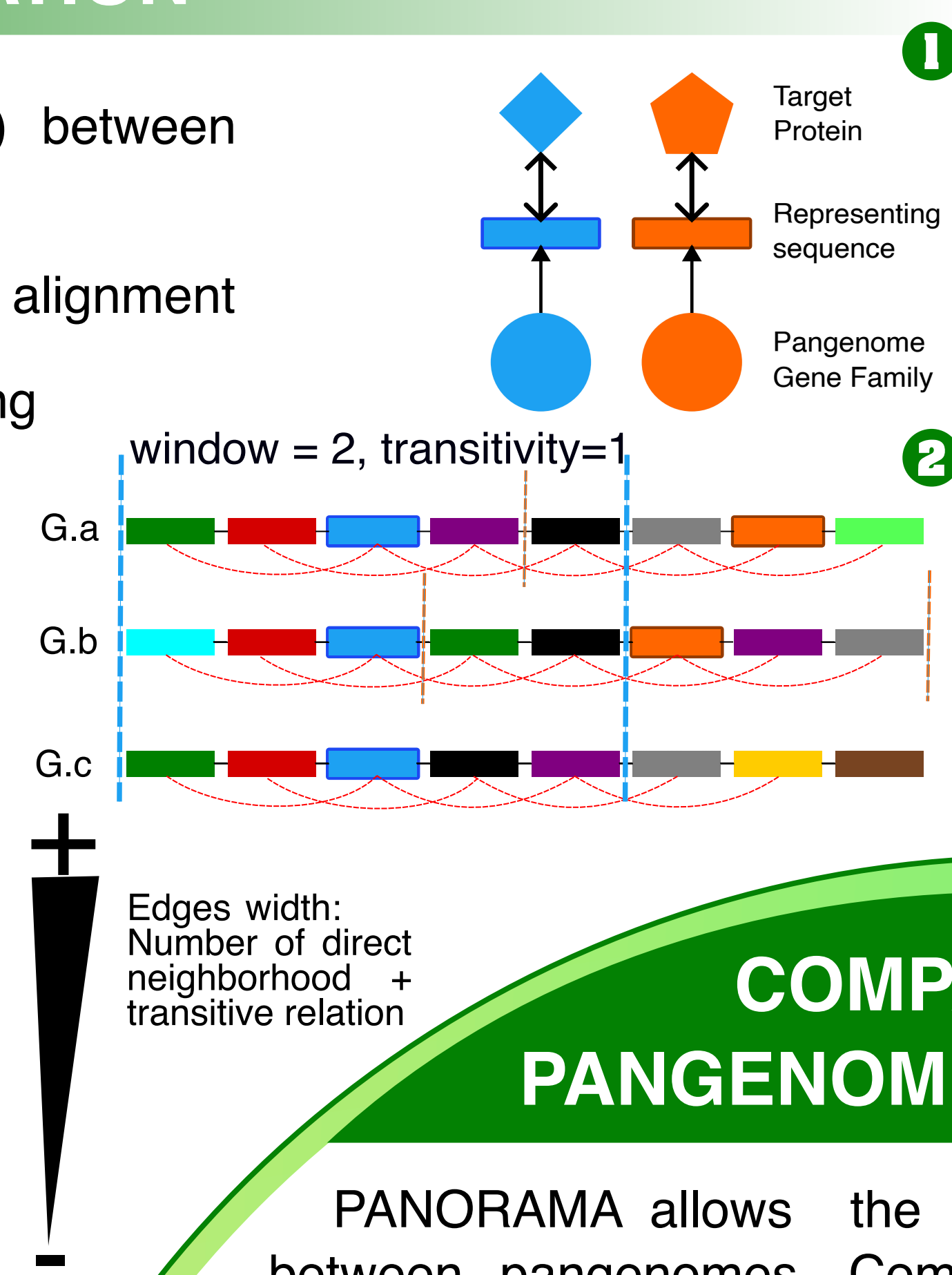
PANORAMA aims to help microbiologists understand the adaptive potential of bacteria and, through the exploration of functional modules in different species, to better understand the evolutionary dynamics behind the metabolic diversity of microorganisms.



GENOMIC CONTEXT EXPLORATION

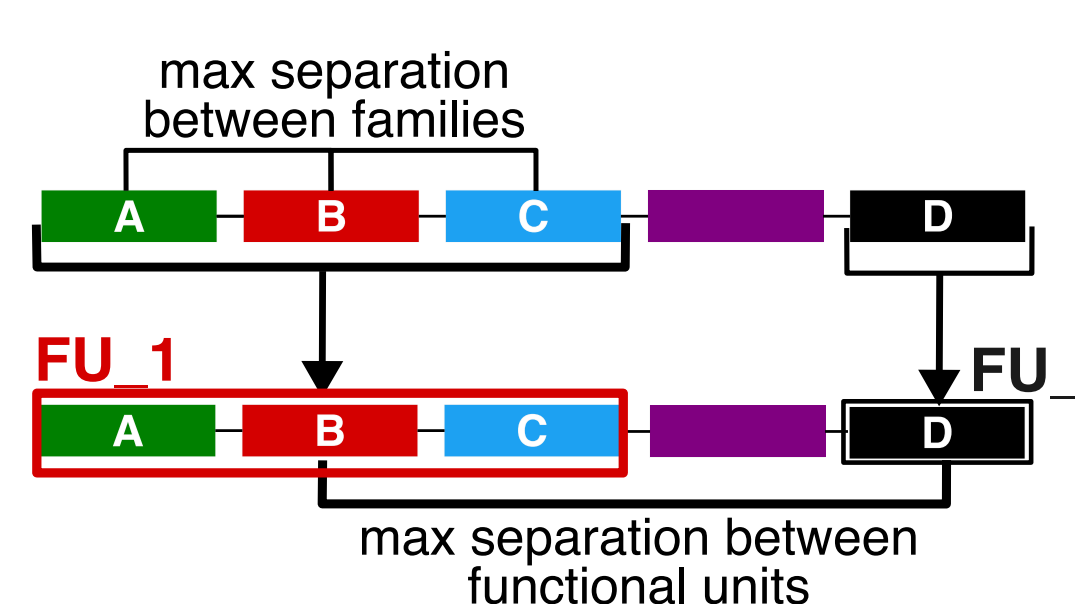
Identify conserved **genomic contexts** (GC) between pangenomes from a set of proteins of interest.

1. Detect homologous families using sequence alignment
2. Search for connected components applying transitive closure and window size parameters
3. GC graph construction.
4. Edges filtering according to a Jaccard index

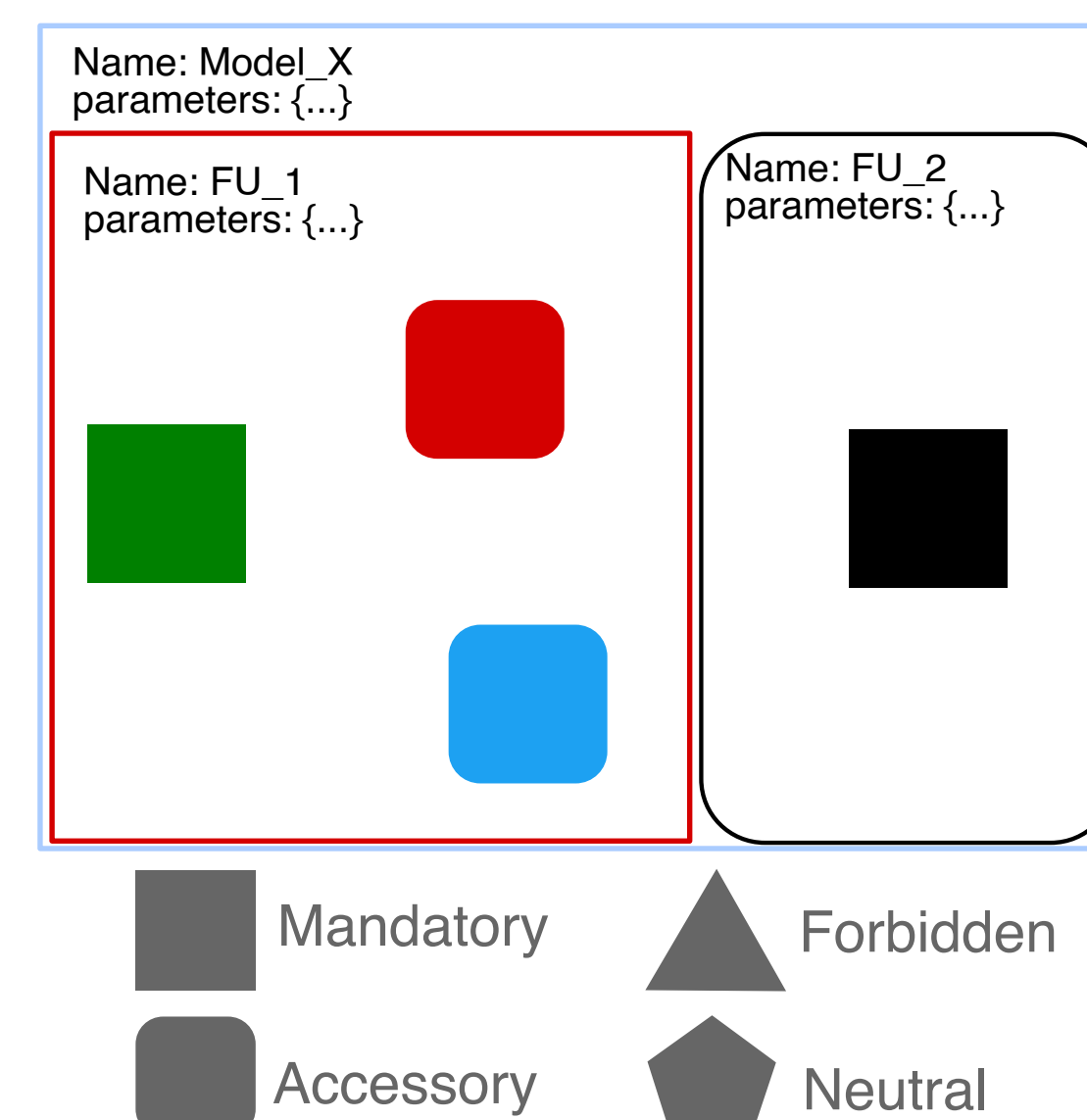


PANORAMA models **biological systems** based on rules which describes gene family presence/absence and synteny conservation, similarly to MacSyFinder⁴.

Model representation in a genome



Model representation schema



Model structure in JSON grammar

```
{
  "name": "model_X",
  "parameters": {
    "max_separation": 1,
    "min_mandatory": 1,
    "min_total": 1
  },
  "func_units": [
    {
      "name": "FU_1",
      "type": "mandatory",
      "parameters": {
        "min_total": 2
      }
    },
    {
      "name": "famA",
      "type": "mandatory"
    },
    {
      "name": "famB",
      "type": "accessory"
    },
    {
      "name": "famC",
      "type": "accessory",
      "parameters": {
        "max_separation": 2
      }
    }
  ]
}
```

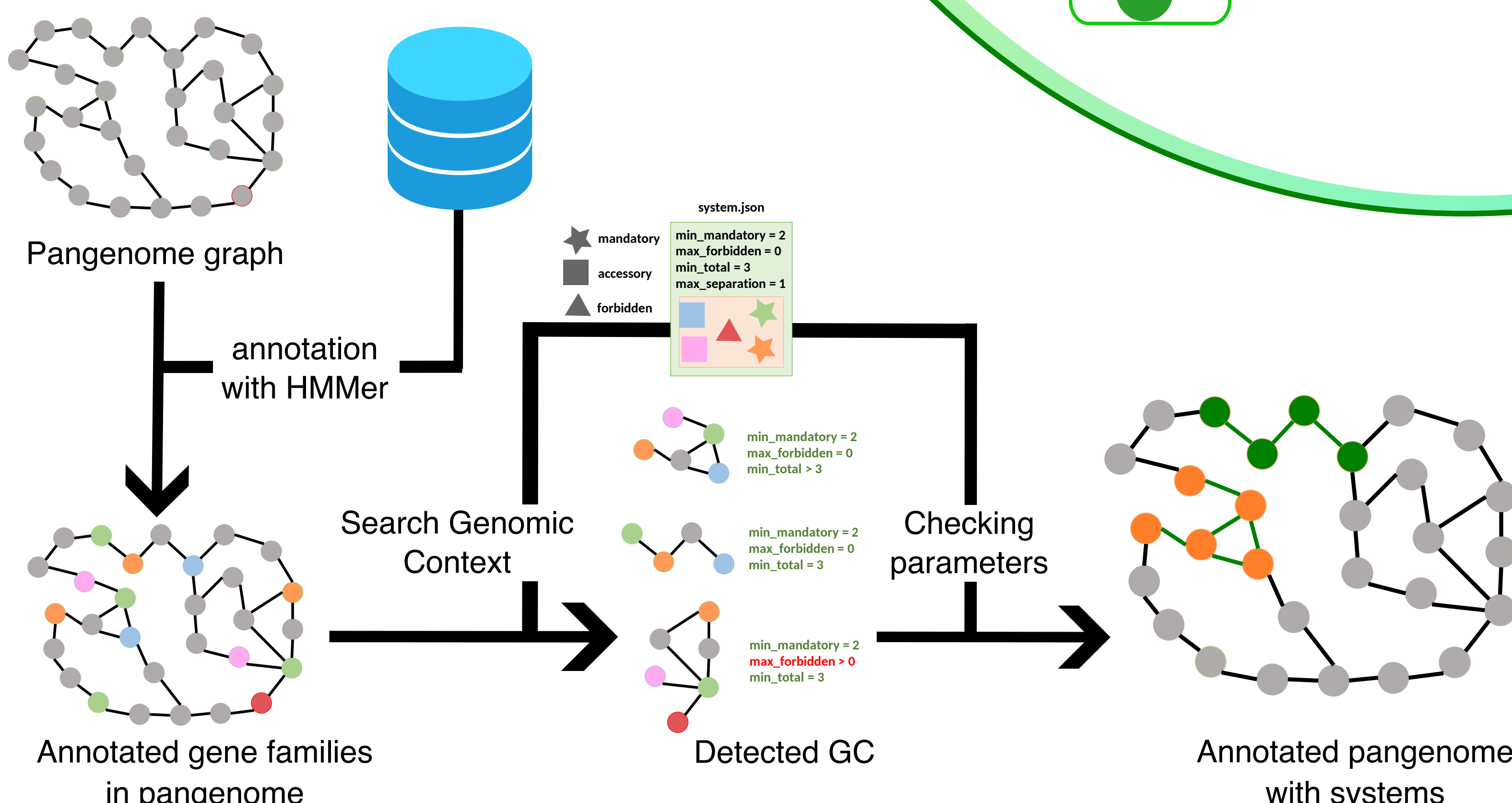
461 models integrated:

- defense(435)
- secretion(26)
- Ongoing systems:
- KEGG modules
- Polysaccharides Utilization Loci

SYSTEM DETECTION

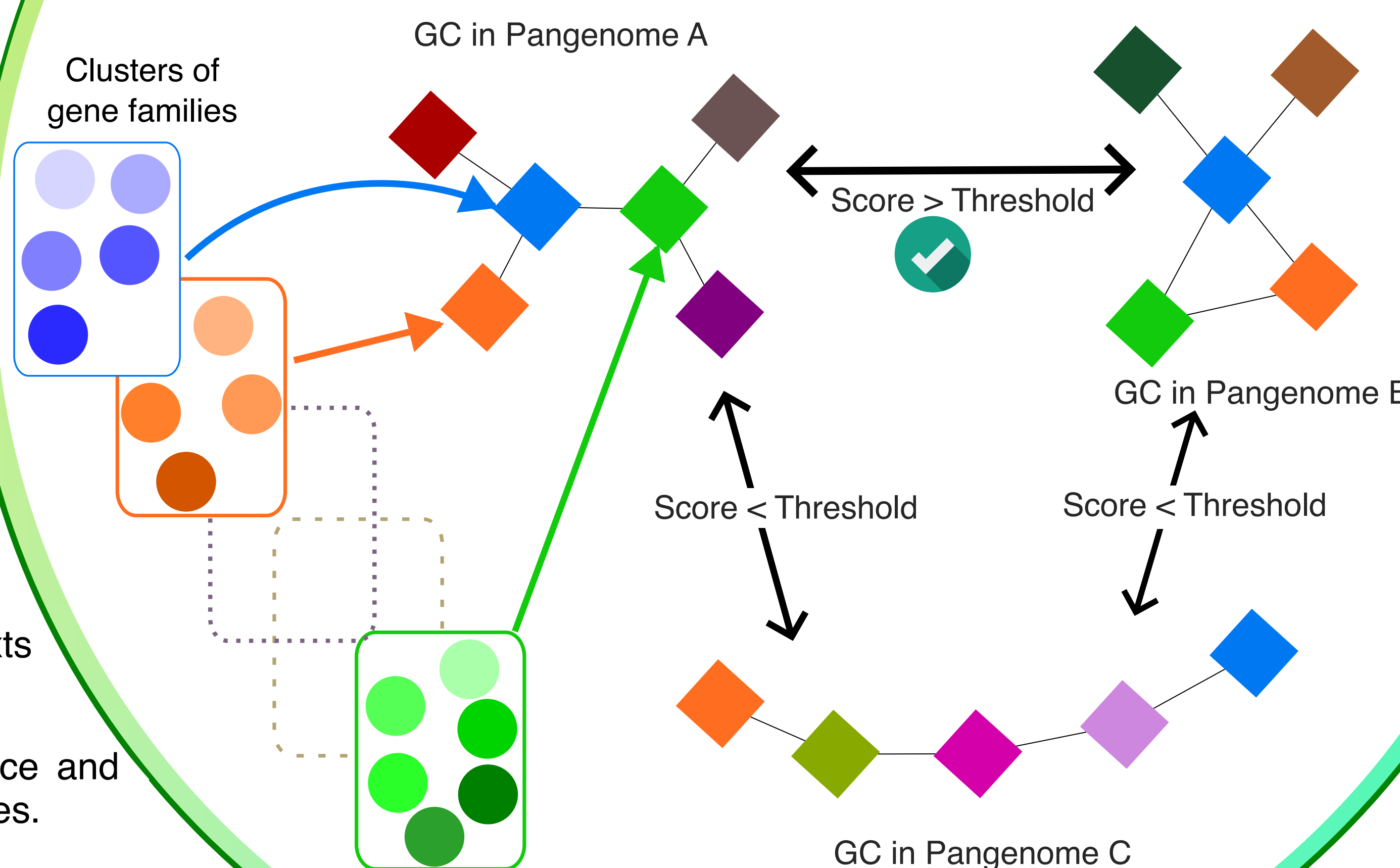
System detection in PANORAMA is based on a functional annotation of gene families, GC searching and system modeling.

1. Annotation of gene families with HMMs associated to system-models
2. Detection of genomic contexts corresponding to the models
3. PANORAMA verifies that presence/absence and synteny parameters fit with the associated rules.



COMPARATIVE PANGENOMICS ANALYSES

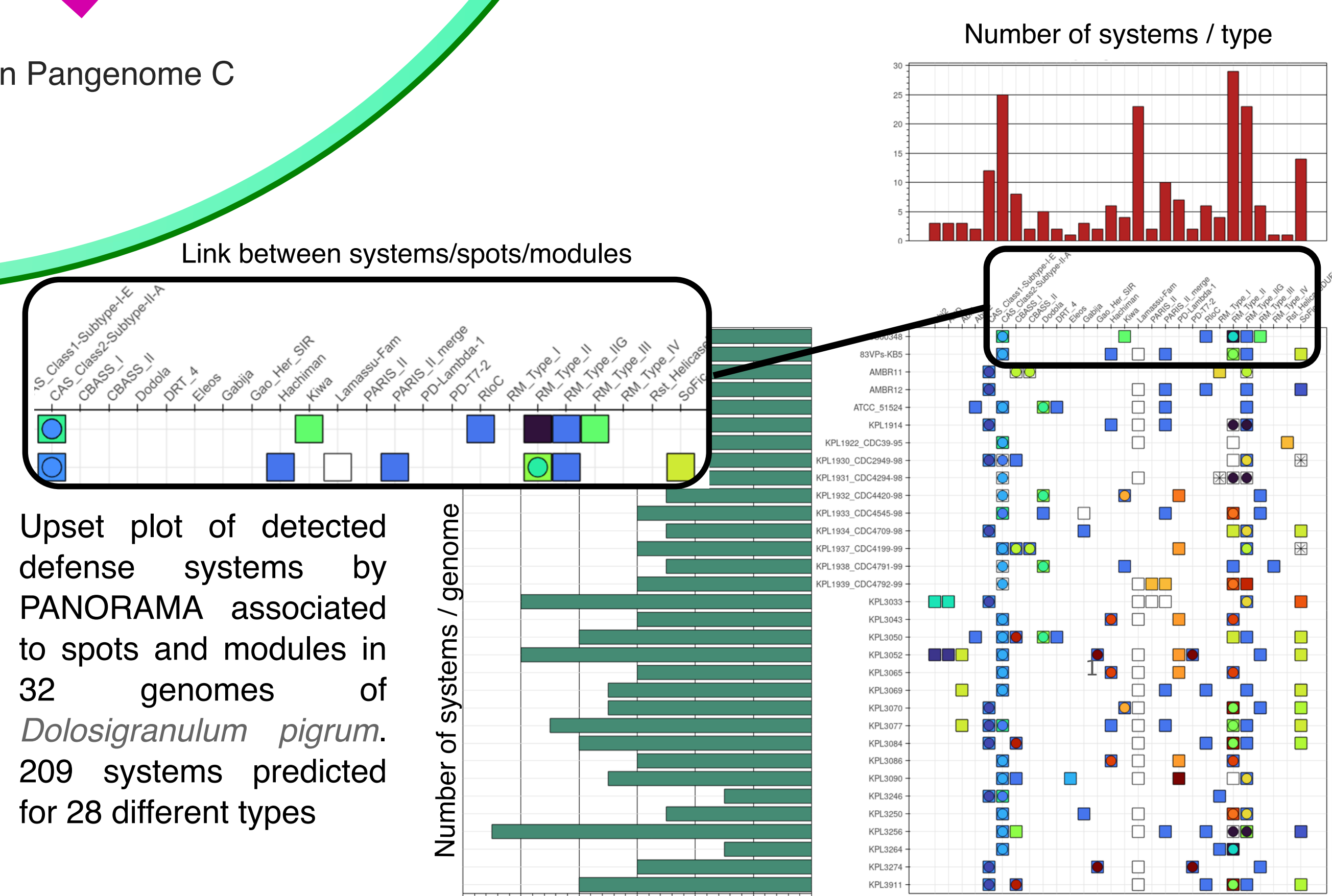
PANORAMA allows the identification of conserved GCs between pangenomes. Comparisons are based on grouping pangenome families and computing common connected components. A conservation score is calculated for each pair of GCs to obtain those that are common and may correspond to pathways or cellular processes conserved between species..



SYSTEM-ASSOCIATION

Systems detected at the pangenome level can be projected to individual genomes and associated to pangenome graph components (partition, region of genomic plasticity², spots² and modules³) and give them a functional annotation.

Using PANORAMA to predict defense systems allow to identify regions of genomic plasticity corresponding to anti-phage defense islands in genomes



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